

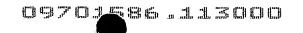
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: BASF Aktiengesellschaft
 - (B) STREET:
 - (C) CITY: Ludwigshafen
 - (E) COUNTRY: Deutschland
 - (F) POSTAL CODE (ZIP): 67065
- (ii) TITLE OF INVENTION: Neue Poly ADP Ribose Polymerase Gene
- (iii) NUMBER OF SEQUENCES: 28
 - (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC DOS/MS DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

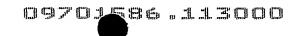
(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
 - (iv) ANTI SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3...1715
 - (D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- CC ATG GCG GCG CGG CGA CGG AGC ACC GGC GGC AGG GCG AGA 47
 Met Ala Ala Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
 1 5 10 15
- GCA TTA AAT GAA AGC AAA AGA GTT AAT AAT GGC AAC ACG GCT CCA GAA 95
 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
 20 25 30



					AAA Lys										143
					GGA Gly										191
					GTG Val 70										239
					ACA Thr										287
					TAT Tyr										335
					TAC Tyr										383
					GTT Val										431
					GTG Val 150										479
					AAA Lys										527
					GAG Glu										575
	Asp	Tyr	Ala	Thr	AAT Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys		623
					CCC Pro										671
					AAG Lys 230										719
					AAG Lys										767
					ATC Ile										815

				260					265					270		
			TGT Cys 275													863
			GAA Glu													911
			CTA Leu													959
			GCT Ala													1007
			CAA Gln													1055
			GCC Ala 355													1103
			CAG Gln													1151
			ACC Thr													1199
			TTC Phe													1247
			ATG Met													1295
			CCT Pro 435													1343
			GCT Ala													1391
			AAG Lys													1439
			AAT Asn													1487
СТТ	CAA	GGT	AAA	CAT	AGC	ACC	AAG	GGG	CTG	GGC	AAG	ATG	GCT	CCC	AGT	1535



Leu	Gln	Gly	Lys	His 500	Ser	Thr	Lys	Gly	Leu 505	Gly	Lys	Met	Ala	Pro 510	Ser	
				GTC Val											CCA Pro	1583
				GGA Gly												1631
				GTA Val												1679
				TTT Phe								ATG'	rtga:	TAT		1725
TAA	ATAA	ACC 2	AGAG	ATCT	GA TO	CTTC	AAGC	A AG	AAAA?	raag	CAG	rgtt(GTA (CTTG	IGAATT	1785
TTG	rgat.	ATT :	TAT	GTAA!	ra ai	AAAC	rgtac	C AG	GTCT1	AAAA	AAA	AAAA	AAA Z	AAAA	AAAA	1843

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 571 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ala Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala 1 5 10 15

Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
20 25 30

Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
35 40 45

Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp 50 55 60

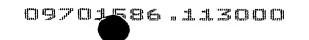
Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro 65 70 75 80

Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys 85 90 95

Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln 100 105 110

Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala 115 120 125

Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met



	130					135					140				
Gly 145	Gln	His	Ser	Leu	Val 150	Ala	Cys	Ser	Gly	Asn 155	Leu	Asn	Lys	Ala	Lys 160
Glu	Ile	Phe	Gln	Lys 165	Lys	Phe	Leu	Asp	Lys 170	Thr	Lys	Asn	Asn	Trp 175	Glu
Asp	Arg	Glu	Lys 180	Phe	Glu	Lys	Val	Pro 185	Gly	Lys	Tyr	Asp	Met 190	Leu	Gln
Met	Asp	Tyr 195	Ala	Thr	Asn	Thr	Gln 200	Asp	Glu	Glu	Glu	Thr 205	Lys	Lys	Glu
Glu	Ser 210	Leu	Lys	Ser	Pro	Leu 215	Lys	Pro	Glu	Ser	Gln 220	Leu	Asp	Leu	Arg
Val 225	Gln	Glu	Leu	Ile	Lys 230	Leu	Ile	Cys	Asn	Val 235	Gln	Ala	Met	Glu	Glu 240
Met	Met	Met	Glu	Met 245	Lys	Tyr	Asn	Thr	Lys 250	Lys	Ala	Pro	Leu	Gly 255	Lys
.Leu	Thr	Val	Ala 260	Gln	Ile	Lys	Ala	Gly 265	Tyr	Gln	Ser	Leu	Lys 270	Lys	Ile
Glu	Asp	Cys 275	Ile	Arg	Ala	Gly	Gln 280	His	Gly	Arg	Ala	Leu 285	Met	Glu	Ala
Cys	Asn 290	Glu	Phe	Tyr	Thr	Arg 295	Ile	Pro	His	Asp	Phe 300	Gly	Leu	Arg	Thr
Pro 305	Pro	Leu	Ile	Arg	Thr 310	Gln	Lys	Glu	Leu	Ser 315	Glu	Lys	Ile	Gln	Leu 320
Leu	Glu	Ala	Leu	Gly 325	Asp	Ile	Glu	Ile	Ala 330	Ile	Lys	Leu	Val	Lys 335	Thr
Glu	Leu	Gln	Ser 340	Pro	Glu	His	Pro	Leu 345	Asp	Gln	His	Tyr	Arg 350	Asn	Leu
His	Cys	Ala 355	Leu	Arg	Pro	Leu	Asp 360	His	Glu	Ser	Tyr	Glu 365	Phe	Lys	Val
Ile	Ser 370	Gln	Tyr	Leu	Gln	Ser 375	Thr	His	Ala	Pro	Thr 380	His	Ser	Asp	Tyr
Thr 385	Met	Thr	Leu	Leu	Asp 390	Leu	Phe	Glu	Val	Glu 395	Lys	Asp	Gly	Glu	Lys 400
Glu	Ala	Phe	Arg	Glu 405	Asp	Leu	His	Asn	Arg 410	Met	Leu	Leu	Trp	His 415	Gly
Ser	Arg	Met	Ser 420	Asn	Trp	Val	Gly	Ile 425	Leu	Ser	His	Gly	Leu 430	Arg	Ile
Ala	Pro	Pro 435	Glu	Ala	Pro	Ile	Thr 440	Gly	Tyr	Met	Phe	Gly 445	Lys	Gly	Ile
Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala	Ser

450 455 460

Arg Leu Lys Asn Thr Gly Leu Leu Leu Ser Glu Val Ala Leu Gly
465 470 475 480

Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu 485 490 495

Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser 500 505 510

Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala 515 520 525

Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn 530 540

Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu 545 550 555 560

Lys Val Gln Phe Asn Phe Leu Gln Leu Trp * 565 570

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 242..1843
 - (D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA 60

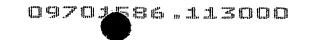
TAGCCGATGT CTAATCCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC 120

TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG 180

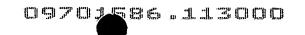
GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATGTCCCTGC TTTTCTTGGC 240

C ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT GAG 286

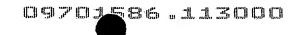
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu



	575		580	585	
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			Pro Ala Glu	G AAG CGC ATA ATC Lys Arg Ile Ile 615	
				GGG ACC CAG GTG Gly Thr Gln Val 630	
		r Leu Asn		C ATC GAG AAC AAC n Ile Glu Asn Asn 5	
				C AGC AAC CGC TTC Ser Asn Arg Phe 665	
				G GTC GGC CAG TCA 1 Val Gly Gln Ser 680	
				G AAG GAC TTT GAG S Lys Asp Phe Glu 695	
				A GAG CGG GAC CAC a Glu Arg Asp His 710	
		s Tyr Thr		A GTA CAG GCA GAG 1 Val Gln Ala Glu 5	
				A GGC CCA GTG AGG g Gly Pro Val Arg 745	
				C CCA GCC ACG CAG Pro Ala Thr Gln 760	
			Glu Met Phe	C AAG AAC ACC ATG e Lys Asn Thr Met 775	
				G GGA AAG CTG AGC u Gly Lys Leu Ser 790	
		y Phe Glu		G GCG CTG GAG GAG u Ala Leu Glu Glu 5	
CTG AAA GGC	CCC ACG GA	T GGT GGC	CAA AGC CTO	G GAG GAG CTG TCC	TCA 1006



Leu	Lys	Gly	Pro	Thr 815	Asp	Gly	Gly	Gln	Ser 820	Leu	Glu	Glu	Leu	Ser 825	Ser		
													CAG Gln 840			10	54
													ATG Met			11	102
Val													GTC Val			11	150
													CGA Arg			11	198
													GCA Ala			12	246
													AAC Asn 920			12	294
													GGG Gly			13	342
													CTG Leu			13	390
													AGT Ser			14	438
													ATC Ile			14	486
													ATG Met 100	Lys		15	534
			His					Phe					GCC Ala 5			15	582
		His					Asp					Lys	AGC Ser			16	630
	Gly					Ile					Thr		CCT Pro			16	678



ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG CCC Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Pro 1055 1060 1065	1726
CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC TCC Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser 1070 1075 1080	1774
CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC TAC Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr 1085 1090 1095	1822
CTG CTG GAG GTC CAC CTC TGA GTGCCCGCCC TGTCCCCCGG GGTCCTGCAA Leu Glu Val His Leu * 1100 1105	1873
GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT	1933
TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA	1993
CTTATGCCTC CTAACTGAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC	2053
CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC	2113
ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT	2173
AATGTGCACC GGGTTCACCC ATGTTTTCAT AAATGACAAG ATTTCCTCCT TTAAAAAAAA	2233
AAAAAAAAA AAAAAAAAA AA	2265

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys

1 10 15

Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr 20 25 30

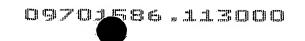
Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val

Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
50 60

Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn 65 70 75 80

Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr 85 90 95

Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile



100 105 110 Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys 120 Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val 130 Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu 200 Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln 215 Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His 250 Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val 280 Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln 295 Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln 305 Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr 325 330 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys 340 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Asp 360 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His 370 Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg 395 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly

420

430

Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro
450
Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
465
Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
485
Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln

425

Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
515 520 525

Leu Glu Val His Leu * 530

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 221..1843
 - (D) OTHER INFORMATION:/product= "Poly ADP Ribose Polymerase"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA 60

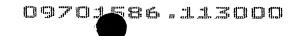
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TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG 180

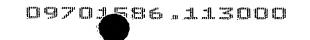
GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATG TCC CTG CTT TTC 235

Met Ser Leu Leu Phe 535

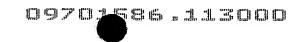
TTG GCC ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT 283



Leu 540	Ala	Met	Ala	Pro	Lys 545	Pro	Lys	Pro	Trp	Val 550	Gln	Thr	Glu	Gly	Pro 555	
					CGG Arg											331
					CTC Leu											379
-					TGT Cys											427
					TGC Cys											475
					ATC Ile 625											523
					CGC											571
					ACA Thr											619
					AAG Lys											667
					GGC Gly											715
					GCT Ala 705									_		763
					GTG Val											811
					ATC Ile											859
					GAT Asp											907
					CGG Arg										GAG Glu	955



	CTG Leu								1003
-	CAC His								1051
	CCC Pro								1099
	GTG Val								1147
	CAG Gln 845								1195
	CAG Gln	 							1243
	TAC Tyr								1291
	TGC Cys								1339
	GAC Asp								1387
	CAT His 925								1435
	CGC Arg								1483
	GCC Ala								1531
	GGG Gly								1579
	AGA Arg						Lys		1627
	CCT Pro								1675



1015 1005 1010 CCG ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG 1723 Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val 1020 1025 1030 1035 CCC CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC 1771 Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe 1040 1045 1050 TCC CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC 1819 Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg 1065 1055 1060 TAC CTG CTG GAG GTC CAC CTC TGA GTGCCCGCCC TGTCCCCCGG GGTCCTGCAA 1873 Tyr Leu Leu Glu Val His Leu * 1075 1070 GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT 1933 TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA 1993 CTTATGCCTC CTAACTGAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC 2053 CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC 2113 ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT 2173 AATGTGCACC GGGTTCACCC ATGTTTTCAT AAATGACAAG ATTTCCTCCT TTAAAAAAAA 2233 2265 ΑΑΑΑΑΑΑΑΑ ΑΑΑΑΑΑΑΑΑ ΑΑΑΑΑΑΑΑΑ ΑΑ (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 541 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val 1 5 10 15

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu 20 25 30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala 35 40 45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn 50 55 60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr 65 70 75 80

Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln

85 90 95

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly
100 105 110

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala 115 120 125

Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp 130 135

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile 145 150 155 160

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp 165 170 175

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met 195 200 205

Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro 210 215 220

Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu 225 230 235 240

Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser 245 250 255

Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe 260 265 270

Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala 275 280 285

Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala 290 295 300

Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His 305 310 315 320

Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu 325 330 335

Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln 340 345 350

Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val 355 360 365

Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly 370 375 380

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala 385 390 395 400

Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val

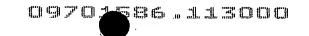
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				405					410					415		
Gly	Lys	Gly	Ile 420	Tyr	Phe	Ala	Ser	Glu 425	Asn	Ser	Lys	Ser	Ala 430	Gly	Tyr	
Val	Ile	Gly 435	Met	Lys	Cys	Gly	Ala 440	His	His	Val	Gly	Tyr 445	Met	Phe	Leu	
Gly	Glu 450	Val	Ala	Leu	Gly	Arg 455	Glu	His	His	Ile	Asn 460	Thr	Asp	Asn	Pro .	
Ser 465	Leu	Lys	Ser	Pro	Pro 470	Pro	Gly	Phe	Asp	Ser 475	Val	Ile	Ala	Arg	Gly 480	
His	Thr	Glu	Pro	Asp 485	Pro	Thr	Gln	Asp	Thr 490	Glu	Leu	Glu	Leu	Asp 495	Gly	
Gln	Gln	Val	Val 500	Val	Pro	Gln	Gly	Gln 505	Pro	Val	Pro	Cys	Pro 510	Glu	Phe	
Ser	Ser	Ser 515	Thr	Phe	Ser	Gln	Ser 520	Glu	Tyr	Leu	Ile	Tyr 525	Gln	Glu	Ser	
Gln	Cys 530	Arg	Leu	Arg	Tyr	Leu 535	Leu	Glu	Val	His	Leu 540	*				
(2)	INFO	RMA	NOI	FOR	SEQ	ID N	10: 7	7:								
	•	(QUENCA) LE B) TY C) ST C) TC	ENGTE (PE: (RANI (POL)	H: 17 nucl DEDNI DGY:	740 k Leic ESS: line	ase acio sino ear	pai:	s							
	•		LECUI				4									
(отне			NO										
	,		ri se			_										
	` '	(2	IGINA A) OF	RGAN			musc	culus	5							
	(ix)	(2	ATURE A) NA B) LO	ME/I			.1710)								
	(xi)	SEC	QUENC	CE DE	ESCR	[PTIC	on: s	SEQ :	ID NO): 7:	:					
ccc	GCT	TTC A	ACTTI	TTCT	rg C	rgcci	rcgg	G GA	ACAC	CTCG	AGC	CAAC!	rgc :	rtcc:	TAACTC	6
AGG	GTGG	GCA (GAACT	rgaco	GG G	ATCT	AAGC	r TC	rgca:	TCTC	TGA	GGAG	AAC (G GCT t Ala	11
CCA	AAA	CGA	AAG	GCC	TCT	GTG	CAG	ACT	GAG	GGC	TCC	AAG	AAG	CAG	CGA	16

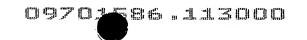
555

Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg

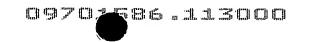
550



		GAG Glu							213
		CCT Pro							261
		CGG Arg 595							309
		CAG Gln							357
		CTG Leu							405
		GGA Gly							453
		GCA Ala							501
		TGG Trp 675							549
		ATA Ile							597
		TTA Leu							645
		TGC Cys							693
		AAA Lys							741
		AAG Lys 755							789
		GAG Glu							837
		GGC Gly							885



	785					790					795					
	ATC Ile															933
	GAT Asp															981
	GAG Glu															1029
	GTG Val															1077
	TGC Cys 865															1125
	CAG Gln															1173
	CGG Arg															1221
	GCC Ala															1269
	GTG Val															1317
	CAC His 945															1365
	AGC Ser															1413
	GTG Val															1461
	ATC Ile								Lys					Gly		1509
	AGC Ser		Ile					Thr					Ala			1557
ATT	GAA	CTT	GAA	CTG	GAT	GGG	CAG	CCG	GTG	GTG	GTG	CCC	CAA	GGC	CCG	1605



Ile	Glu 1025	Leu	Glu	Leu	Asp	Gly 1030		Pro	Val	Val	Val 1035	Gln	Gly	Pro	
	Val	CAG Gln				Phe					Phe				1653
		ATA Ile			Glu					Leu				Glu	1701
	CAC His	CTC Leu	TAAC	GCTGC	CTT C	GCCC	rccci	ra go	STCC	AAGC	2				1740

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

150

165

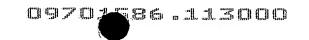
- (A) LENGTH: 533 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

				E TY			ein ON: S	SEQ I	D NO): 8:	:				
Met 1	Ala	Pro	Lys	Arg 5	Lys	Ala	Ser	Val	Gln 10	Thr	Glu	Gly	Ser	Lys 15	Lys
Gln	Arg	Gln	Gly 20	Thr	Glu	Glu	Glu	Asp 25	Ser	Phe	Arg	Ser	Thr 30	Ala	Glu
Ala	Leu	Arg 35	Ala	Ala	Pro	Ala	Asp 40	Asn	Arg	Val	Ile	Arg 45	Val	Asp	Pro
Ser	Cys 50	Pro	Phe	Ser	Arg	Asn 55	Pro	Gly	Ile	Gln	Val 60	His	Glu	Asp	Tyr
Asp 65	Cys	Thr	Leu	Asn	Gln 70	Thr	Asn	Ile	Gly	Asn 75	Asn	Asn	Asn	Lys	Phe 80
Tyr	Ile	Ile	Gln	Leu 85	Leu	Glu	Glu	Gly	Ser 90	Arg	Phe	Phe	Cys	Trp 95	Asn
Arg	Trp	Gly	Arg 100	Val	Gly	Glu	Val	Gly 105	Gln	Ser	Lys	Met	Asn 110	His	Phe
Thr	Cys	Leu 115	Glu	Asp	Ala	Lys	Lys 120	Asp	Phe	Lys	Lys	Lys 125	Phe	Trp	Glu
Lys	Thr 130	Lys	Asn	Lys	Trp	Glu 135	Glu	Arg	Asp	Arg	Phe 140	Val	Ala	Gln	Pro
Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile

155



			180					185					190		
Thr	Asn	Ile 195	Phe	Ser	Lys	Glu	Met 200	Phe	Lys	Asn	Ala	Met 205	Thr	Leu	Met
Asn	Leu 210	Asp	Val	Lys	Lys	Met 215	Pro	Leu	Gly	Lys	Leu 220	Thr	Lys	Gln	Gln
Ile 225	Ala	Arg	Gly	Phe	Glu 230	Ala	Leu	Glu	Ala	Leu 235	Glu	Glu	Ala	Met	Lys 240
Asn	Pro	Thr	Gly	Asp 245	Gly	Gln	Ser	Leu	Glu 250	Glu	Leu	Ser	Ser	Cys 255	Phe
Tyr	Thr	Val	Ile 260	Pro	His	Asn	Phe	Gly 265	Arg	Ser	Arg	Pro	Pro 270	Pro	Ile
Asn	Ser	Pro 275	Asp	Val	Leu	Gln	Ala 280	Lys	Lys	Asp	Met	Leu 285	Leu	Val	Leu
Ala	Asp 290	Ile	Glu	Leu	Ala	Gln 295	Thr	Leu	Gln	Ala	Ala 300	Pro	Gly	Glu	Glu
Glu 305	Glu	Lys	Val	Glu	Glu 310	Val	Pro	His	Pro	Leu 315	Asp	Arg	Asp	Tyr	Gln 320
Leu	Leu	Arg	Cys	Gln 325	Leu	Gln	Leu	Leu	Asp 330	Ser	Gly	Glu	Ser	Glu 335	Tyr
Lys	Ala	Ile	Gln 340	Thr	Tyr	Leu	Lys	Gln 345	Thr	Gly	Asn	Ser	Tyr 350	Arg	Cys
Pro	Asn	Leu 355	Arg	His	Val	Trp	Lys 360	Val	Asn	Arg	Glu	Gly 365	Glu	Gly	Asp
Arg	Phe 370	Gln	Ala	His	Ser	Lys 375	Leu	Gly	Asn	Arg	Arg 380	Leu	Leu	Trp	His
Gly 385	Thr	Asn	Val	Ala	Val 390	Val	Ala	Ala	Ile	Leu 395	Thr	Ser	Gly	Leu	Arg 400
Ile	Met	Pro	His	Ser 405	Gly	Gly	Arg	Val	Gly 410	Lys	Gly	Ile	Tyr	Phe 415	Ala
Ser	Glu	Asn	Ser 420	Lys	Ser	Ala	Gly	Tyr 425	Val	Thr	Thr	Met	His 430	Cys	Gly
Gly	His	Gln 435	Val	Gly	Tyr	Met	Phe 440	Leu	Gly	Glu	Val	Ala 445	Leu	Gly	Lys
Glu	His 450	His	Ile	Thr	Ile	Asp 455	Asp	Pro	Ser	Leu	Lys 460	Ser	Pro	Pro	Pro
Gly 465	Phe	Asp	Ser	Val	Ile 470	Ala	Arg	Gly	Gln	Thr 475	Glu	Pro	Asp	Pro	Ala 480
Gln	Asp	Ile	Glu	Leu 485	Glu	Leu	Asp	Gly	Gln 490	Pro	Val	Val	Val	Pro 495	Gln
Gly	Pro	Pro	Val	Gln	Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln



500 505 510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu 515 520 525

Leu Glu Ile His Leu 530

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) :ORGANISM: Mus .musculus
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...1584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

			GCC Ala 540					48
 			GAG Glu					96
			GCT Ala					144
 	 	 	AAC Asn	 				192
			ACC Thr					240
	 		GAG Glu 620					288
			GAG Glu					336



	GAA Glu							384
	AAC Asn 665							432
	ACA Thr							480
	AAG Lys							528
	GAC Asp							576
	TTC Phe							624
	TTG Leu 745							672
	GAA Glu							720
	CTG Leu							768
	GGC Gly							816
	AAG Lys							864
	TTG Leu 825							912
	CAC His							960
	CTG Leu							1008
	CAG Gln							1056



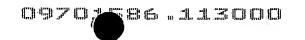
870	875	880	885
Val Trp Lys Val A		GAG GGA GAC AGG TTC CA Glu Gly Asp Arg Phe Gl 895	
	sn Arg Arg Leu I	CTG TGG CAC GGC ACC AA Leu Trp His Gly Thr As 910 91	n Val Ala
		GGG CTC CGA ATC ATG CC Gly Leu Arg Ile Met Pr 930	
		TAT TTT GCC TCT GAG AA Tyr Phe Ala Ser Glu As 945	
		CAC TGT GGG GGC CAC CA His Cys Gly Gly His Gl 960	
Tyr Met Phe Leu C		CTC GGC AAA GAG CAC CA Leu Gly Lys Glu His Hi 975	
	er Leu Lys Ser H	CCA CCC CCT GGC TTT GA Pro Pro Pro Gly Phe As 990 99	p Ser Val
		GAT CCC GCC CAG GAC AT Asp Pro Ala Gln Asp Il 1010	
		GTG CCC CAA GGC CCG CC Val Pro Gln Gly Pro Pr 1025	
		TTC AGC CAG AGT GAA TA Phe Ser Gln Ser Glu Ty 1040	
Tyr Lys Glu Ser (CGC TAC CTG CTG GAG AT Arg Tyr Leu Leu Glu II 1055	
TAA			1587

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys

1 10 15 Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu 25 Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu 155 150 Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser 185 Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys 200 Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp 230 Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val 265 Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln 315 310 Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr



325 330 335

Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His 340 345 350

Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His 355 360 365

Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala 370 380

Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser 385 390 395 400

Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys 405 410 415

Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly
420 425 430

Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr 435 440 445

Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val 450 455 460

Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu 465 470 475 480

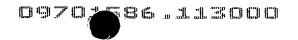
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu 515 520 525

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: YES
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"
- (ix) FEATURE:



- (A) NAME/KEY: Region
- (B) LOCATION: 3
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

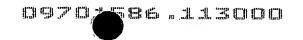
Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:1
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys 1 10 15

Gly Ile Tyr Phe Ala 20

- (2) INFORMATION FOR SEQ ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:



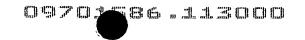
- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:16
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:21
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:24
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:25
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly 20 25 30

Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa Tyr 35 40 45

- (2) INFORMATION FOR SEQ ID NO: 14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: YES
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:1
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Leu oder Val"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa 1 10 15

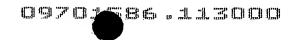
Xaa Xaa Xaa Xaa Leu 20

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:21
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Asp oder Glu"
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION:22
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer 10 oder 11 andere Aminosaeuren"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa 1 10 15

Gln Leu Leu Xaa Xaa Xaa Trp Gly Arg Val Gly
20 25

- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Lys Thr Xaa Asn Xaa 1 5 10 15

Trp Xaa Xaa Xaa Xaa Phe Xaa Xaa Pro Xaa Lys 20 25

- (2) INFORMATION FOR SEQ ID NO: 17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Leu"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Roo Leu Gly Lys Leu 20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Leu 35 40

- (2) INFORMATION FOR SEQ ID NO: 18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

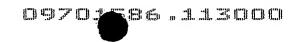
Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 19:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa 1 10 15

Leu

- (2) INFORMATION FOR SEQ ID NO: 20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 - Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1 10
- (2) INFORMATION FOR SEQ ID NO: 21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:



- (A) NAME/KEY: Region
- (B) LOCATION:14
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 7 bis 9 andere Aminosaeuren"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Gly Xaa Xaa Ser Xaa Xaa Xaa Gly Xaa Xaa Pro Xaa Leu Xaa 1 10 15

Gly Xaa Xaa Val 20

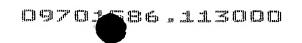
- (2) INFORMATION FOR SEQ ID NO: 22:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION:/note= "Xaa steht fuer Tyr oder Phe"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 23:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Ala Ala Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala 1 5 10 15

Leu Asn Glu Ser



20

- (2) INFORMATION FOR SEQ ID NO: 24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg
1 10 15

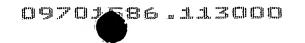
Asn Leu His Cys 20

- (2) INFORMATION FOR SEQ ID NO: 25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr 1 10 15

Ala Glu Ala Leu Lys 20

- (2) INFORMATION FOR SEQ ID NO: 26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:



Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu 1 5 10 15

Glu Ala Leu Lys 20

- (2) INFORMATION FOR SEQ ID NO: 27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu 1 5 10 15

Ala Leu Lys

- (2) INFORMATION FOR SEQ ID NO: 28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu 1 5 10 15

Ala Met Lys